

Figure 1

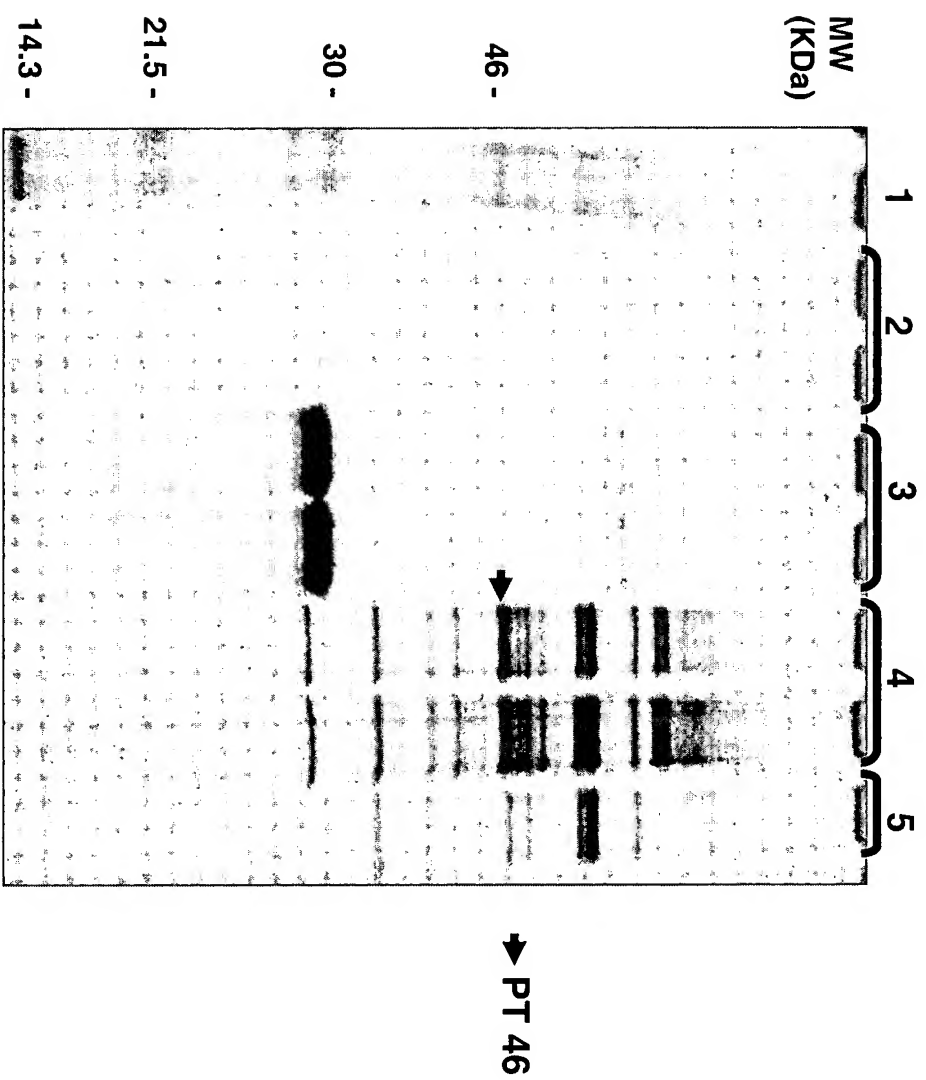


Figure 2

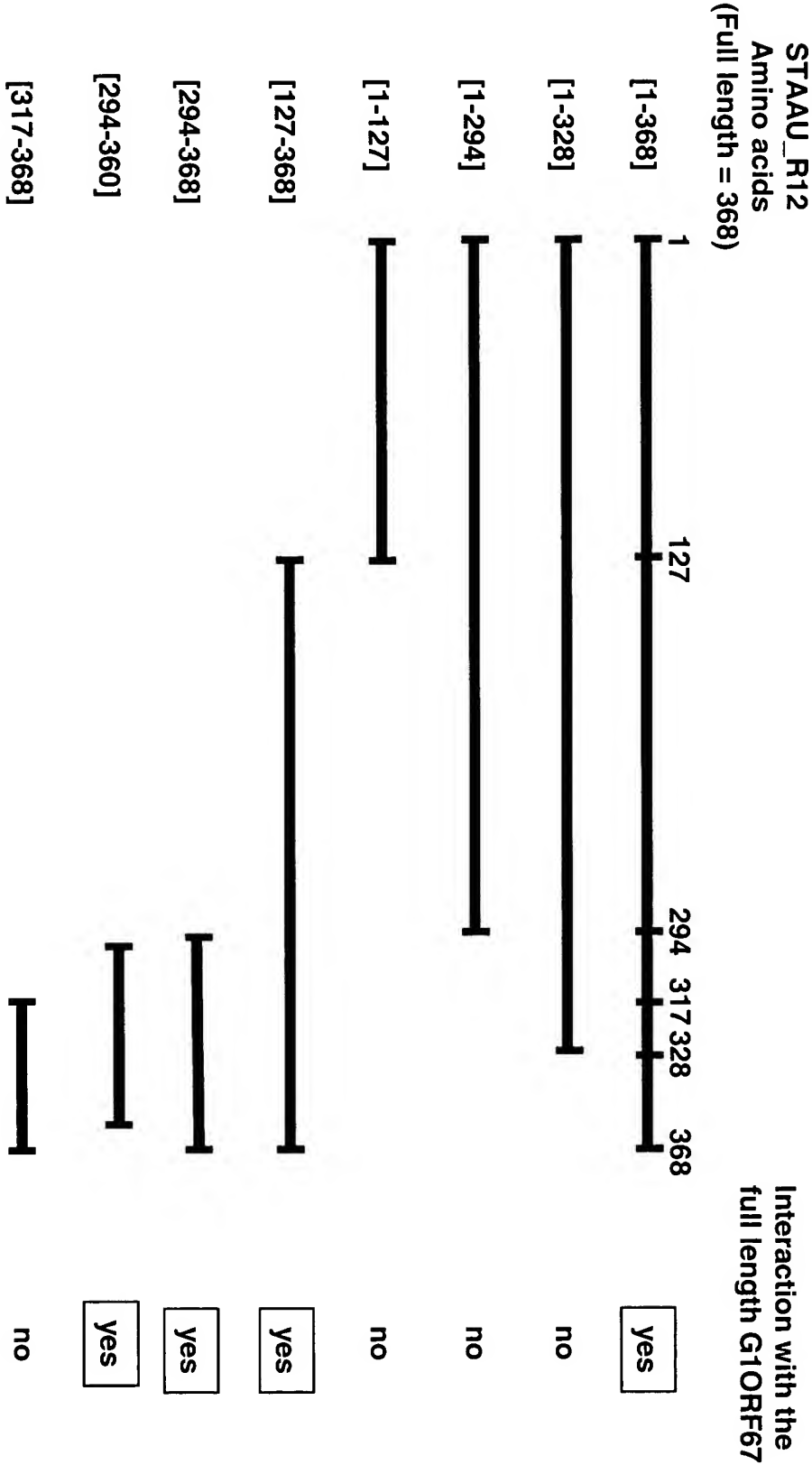
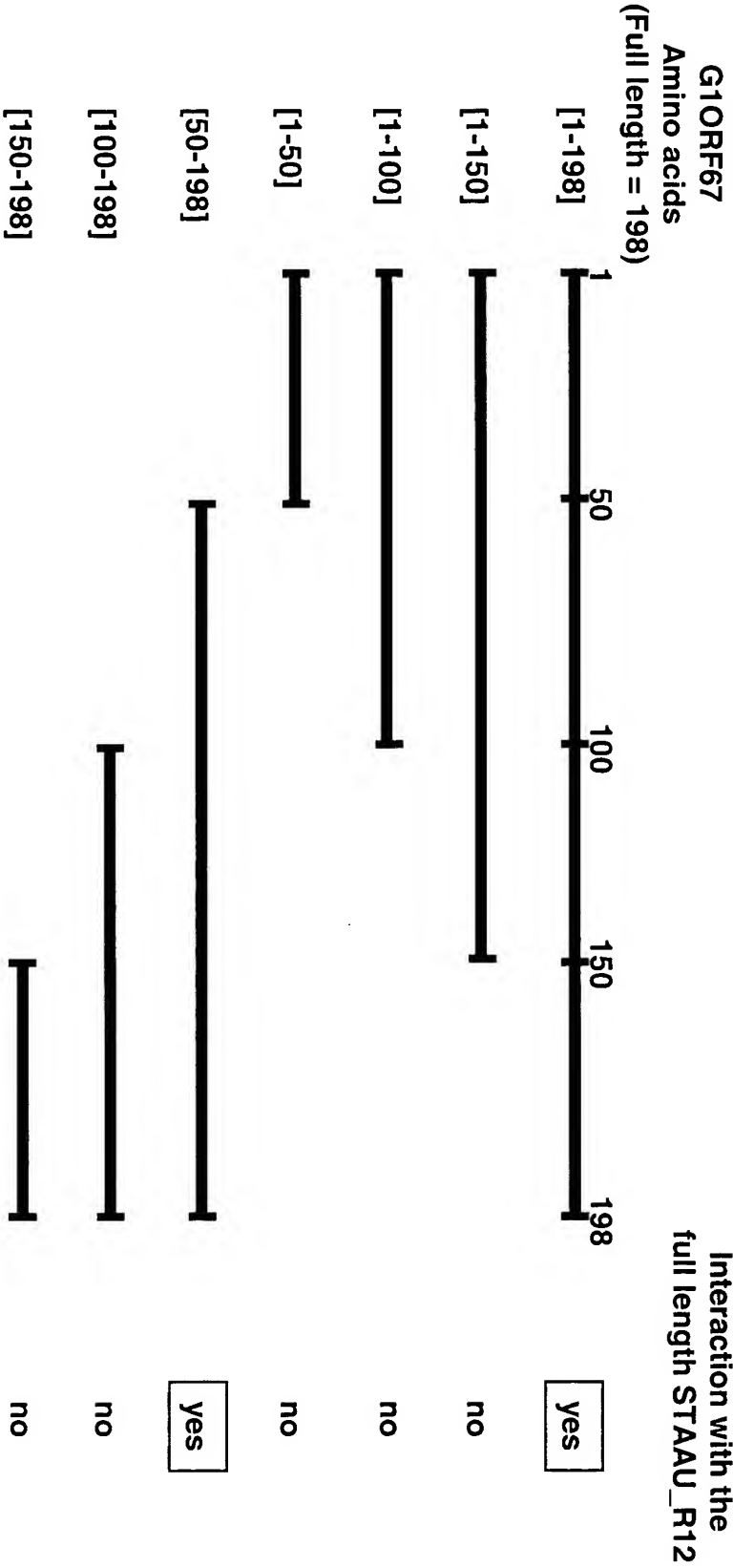
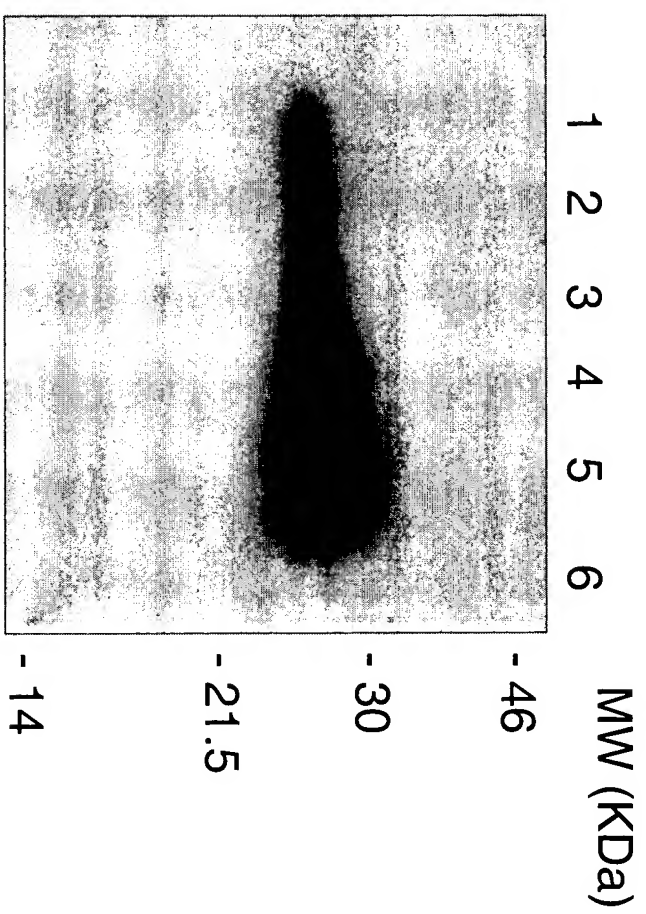


Figure 3A



**Figure 3B**



**Figure 4**

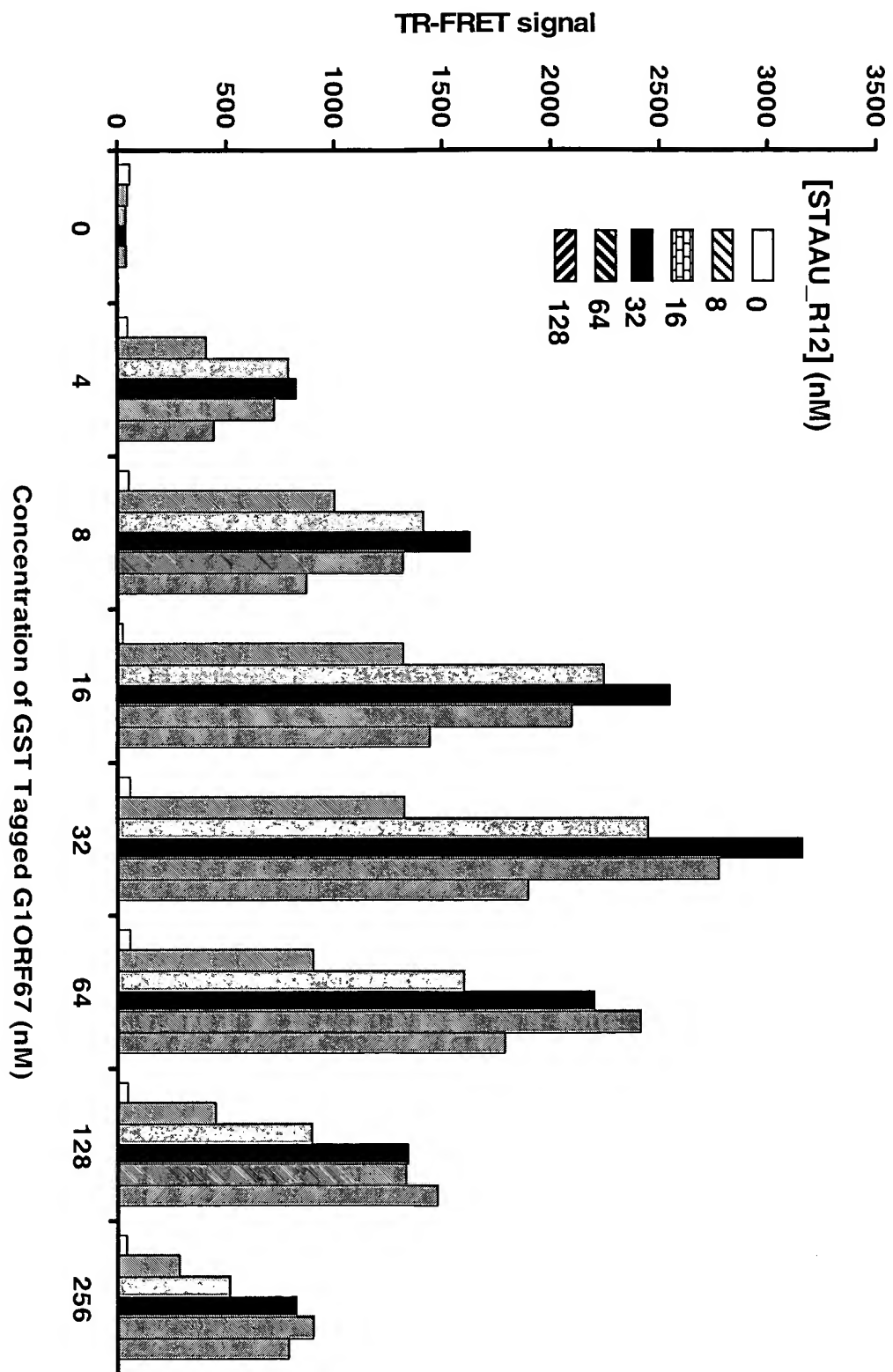


Figure 5A

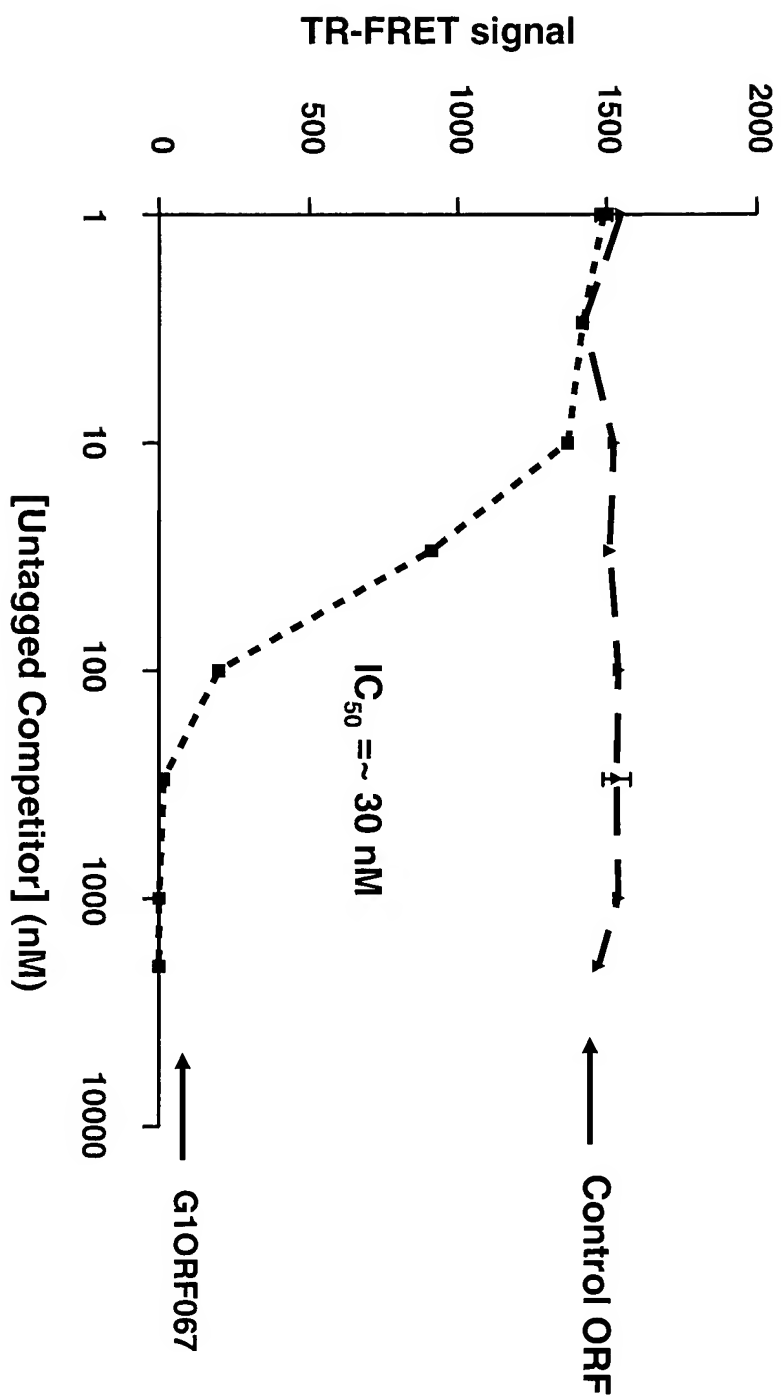
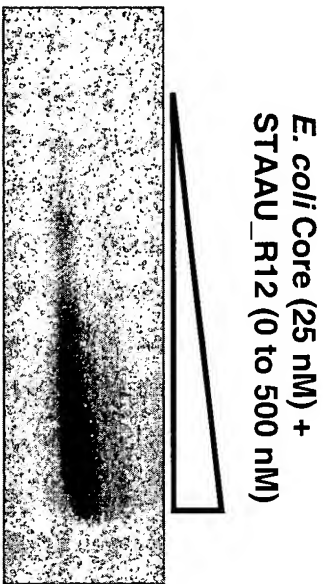
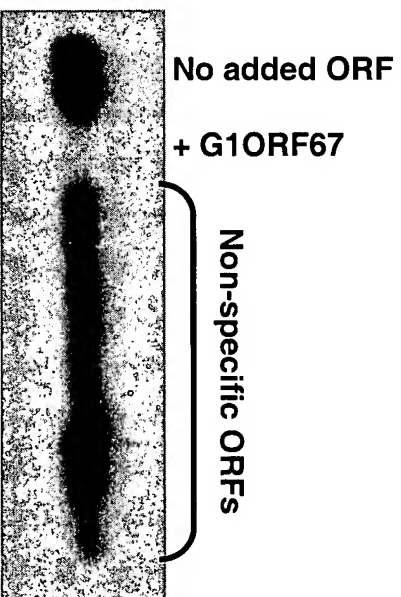


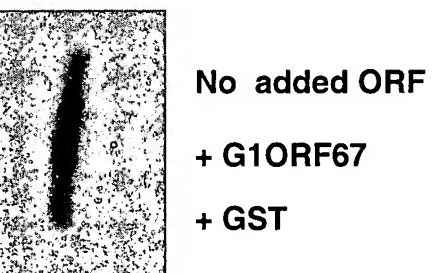
Figure 5B



**Fig. 6A**

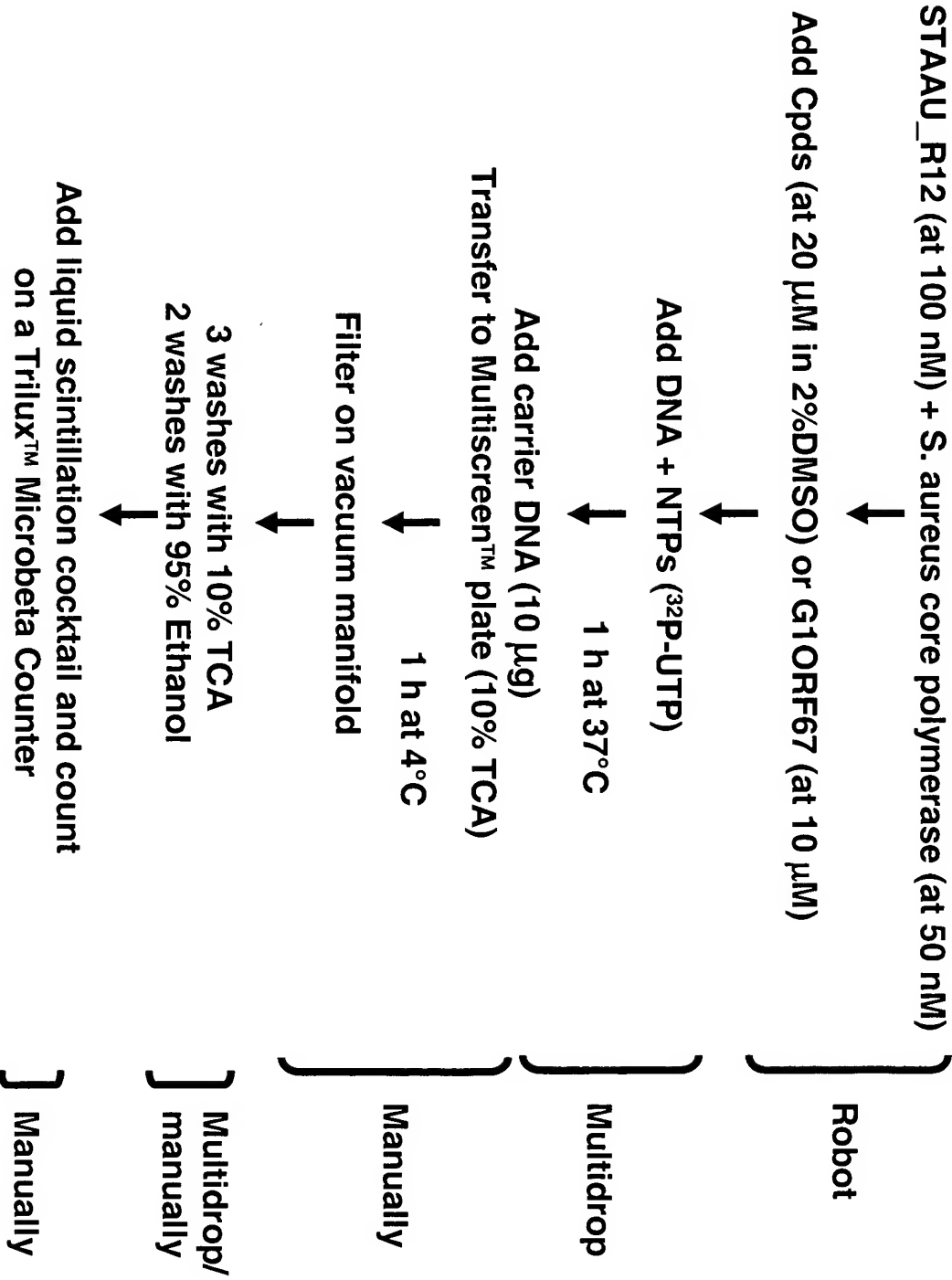


**Fig. 6B**



**Fig. 6C**





**Figure 7**

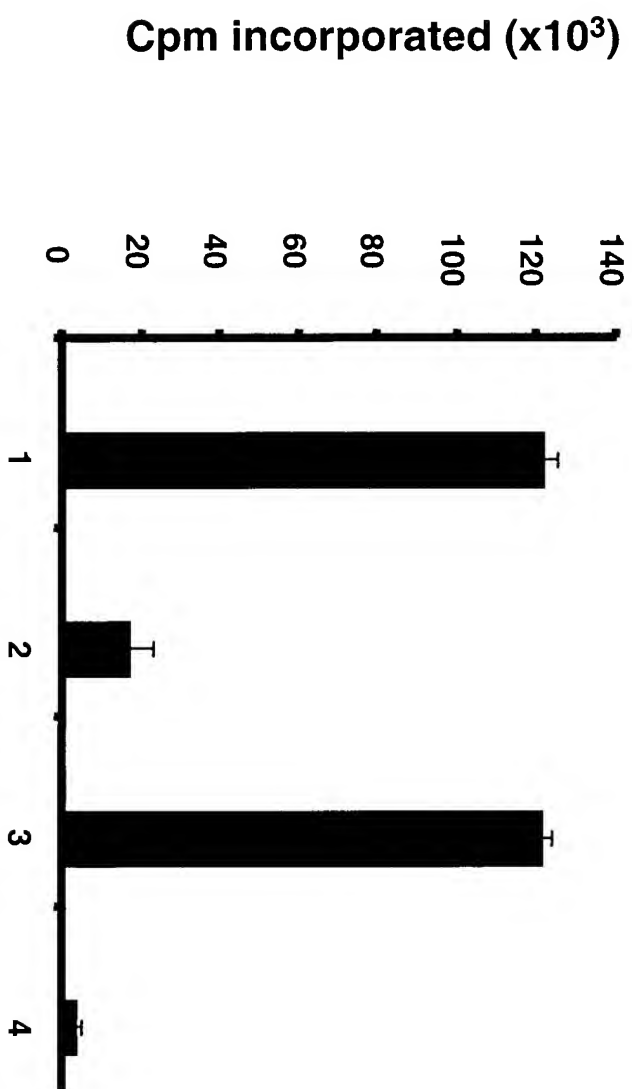
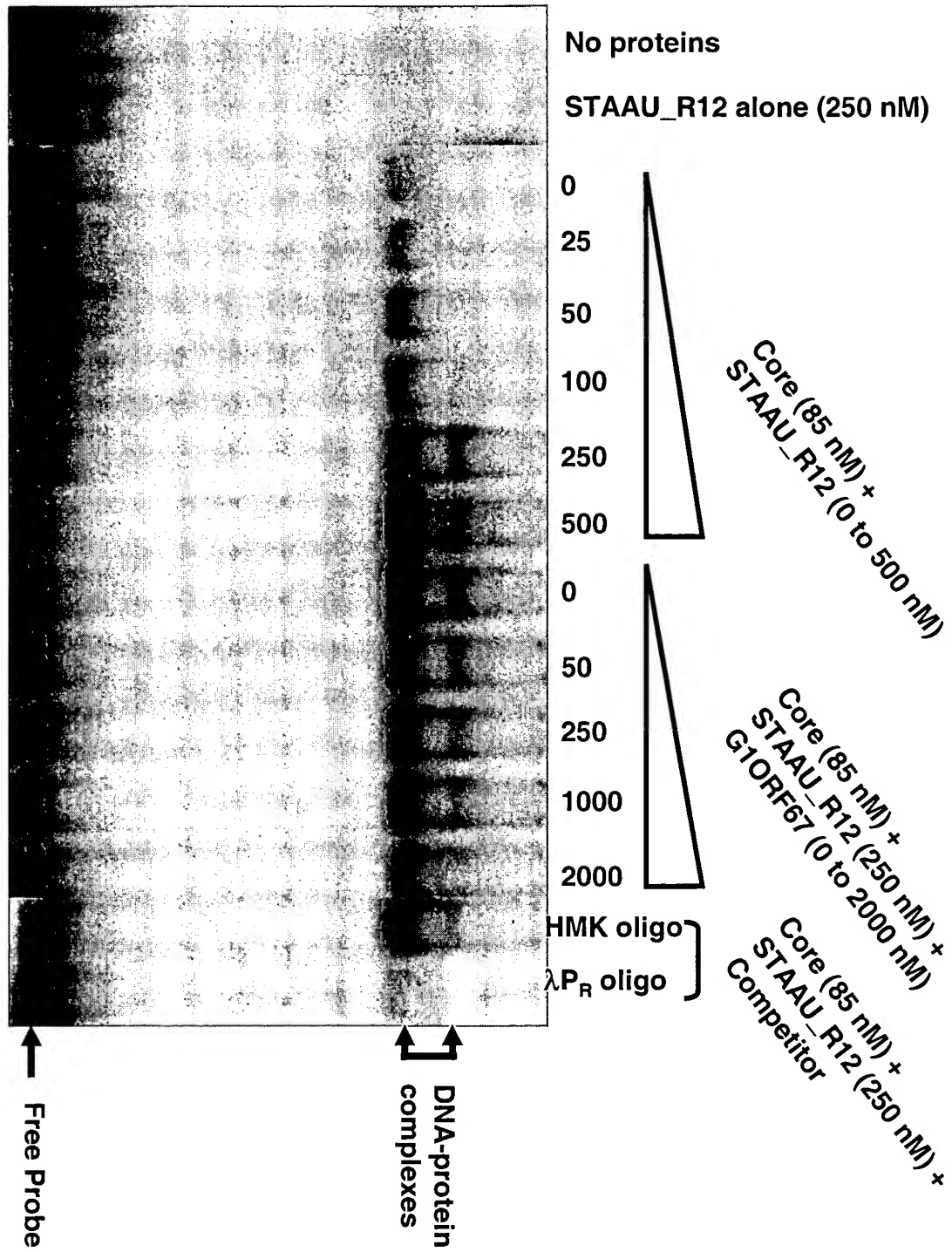


Figure 8

Figure 9



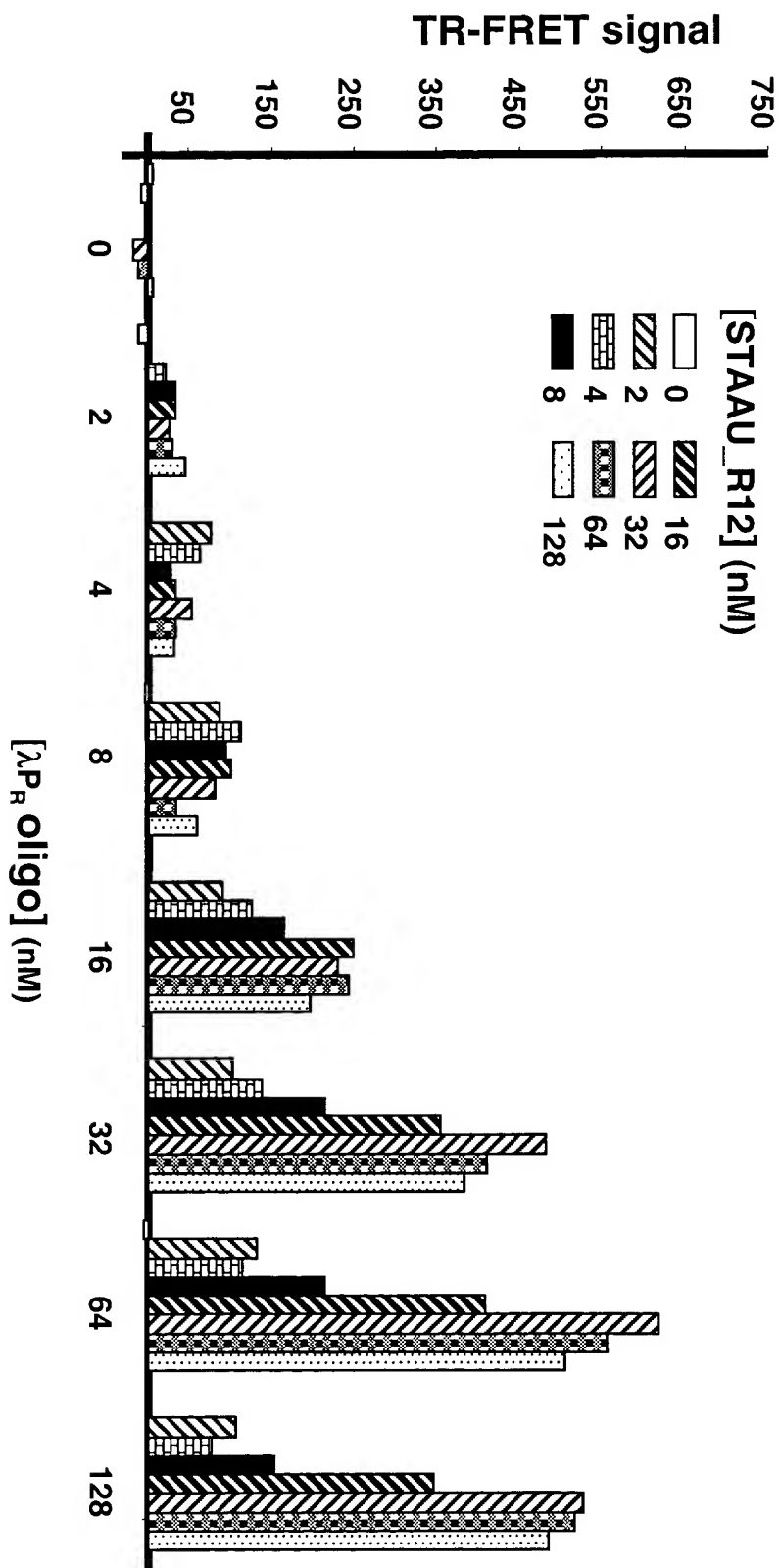
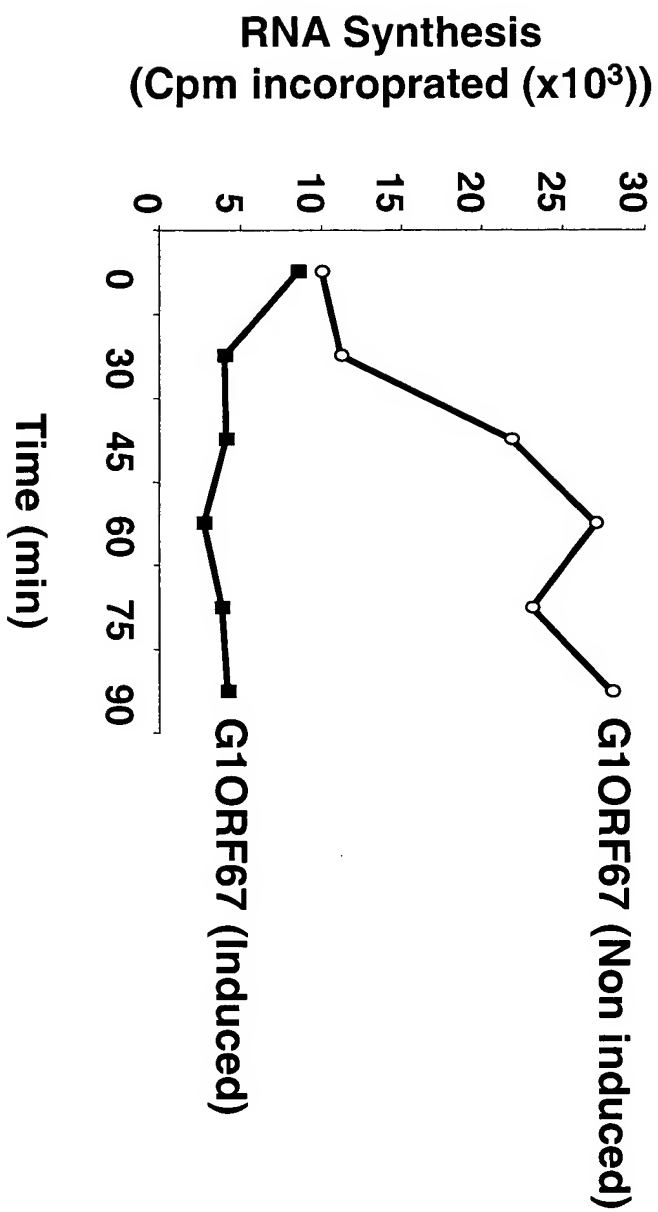


Figure 10



**Figure 11**

**Seq1:** G1ORF067 (SEQ ID NO: 7)  
**Seq2** TwortORF065 (SEQ ID NO: 10)

Substitution matrix: blosum62

Gap penalty: - (11 + 1 \* (gap length))

**Score:** 388

**Identical:** 87/199 (43%), **Similar:** 124/199 (62%), **Gap:** 5/199 (2%)

```

seq1      1 MKLKILDKDNATLNVFHRNKEHKTIDNVPTANLVDWYPLSNAYEYKLSRNGEYLELKRLR   60
          ||||| :|      | |      |      | :|| :|| :||| |||| | | :   : | |||||
seq2      1 MKLKIKNKFMGVLEV--TNSMGVTKLDVPLSNIHEWYPFSNAYSYKYNVKTCDLVLR   58

seq1     61 STLPSSYGLDDNNQDIIRDNNHRCKIGYWYNPAVRKDNLKIIEKAKQYGLPIITEEYDAN  120
          |:| | |||:: ::: | : |      | | :|: || || |||| |||||:| |||:|
seq2     59 SSLPVSYGIERASKEY--DKDKVCNTVTWINHSVKDSNLHIINKAKSYGLPVITEKYTYE  116

seq1    121 TVEQGFRDIGVIFQSLKTIVVTRYLEGKTEEELRIFNMKSEESQLNEALKESDFSVDLTY  180
          |: || : ||| ||::: |||| | : | : |:| : |:::| :: ||
seq2    117 DVDYGFAQLNVIFSELKSLIINRYLEDKDGSFIVKFKRHNPETQYHLAVQDADEVINNTY  176

seq1    181 SDLGQIYNMLLLMKKISK-      198
          :|||:| |||||:|
seq2    177 DELGQMYKMLLLMKKLSKY      195

```

**Figure 12**